

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Gray, John T.
2      Mulligan, Richard C.
3  <120> TITLE OF INVENTION: Packaging Cell Lines
4  <130> FILE REFERENCE: CMCC693p2A
5  <140> CURRENT APPLICATION NUMBER: US/09/393,795
6  <141> CURRENT FILING DATE: 1999-09-10
7  <150> EARLIER APPLICATION NUMBER: US 60/100,063
8  <151> EARLIER FILING DATE: 1998-09-12
9  <150> EARLIER APPLICATION NUMBER: US 60/100,022
10 <151> EARLIER FILING DATE: 1998-09-11
11 <160> NUMBER OF SEQ ID NOS: 12
12 <170> SOFTWARE: FastSEQ for Windows Version 3.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 396
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapien
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20      ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata      180
21      ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat      240
22      acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct      300
23      ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct      360
24      gacacaggac acagcaatca ggtcagccaa aattac      396
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26 <211> LENGTH: 1503
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapien
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30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(1503)
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34      Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp
35      1          5          10          15
36      gaa aaa att cgg tta agg cca ggg gga aag aaa caa tat aaa cta aaa      96
37      Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys
38      20          25          30
39      cat ata gta tgg gca agc agg gag cta gaa cga ttc gca gtt aat cct      144
40      His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
41      35          40          45
42      ggc ctt tta gag aca tca gaa ggc tgt aga caa ata ctg gga cag cta      192
43      Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
44      50          55          60

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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

45	caa cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat	240
46	Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
47	65 70 75 80	
48	aca ata gca gtc ctc tat tgt gtg cat caa agg ata gat gta aaa gac	288
49	Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
50	85 90 95	
51	acc aag gaa gcc tta gat aag ata gag gaa gag caa aac aaa agt aag	336
52	Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
53	100 105 110	
54	aaa aag gca cag caa gca gca gct gac aca gga aac aac agc cag gtc	384
55	Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val	
56	115 120 125	
57	agc caa aat tac cct ata gtg cag aac ctc cag ggg caa atg gta cat	432
58	Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His	
59	130 135 140	
60	cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta gaa	480
61	Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu	
62	145 150 155 160	
63	gag aag gct ttc agc cca gaa gta ata ccc atg ttt tca gca tta tca	528
64	Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser	
65	165 170 175	
66	gaa gga gcc acc cca caa gat tta aat acc atg cta aac aca gtg ggg	576
67	Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly	
68	180 185 190	
69	gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag gaa	624
70	Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu	
71	195 200 205	
72	gct gca gaa tgg gat aga ttg cat cca gtg cat gca ggg cct att gca	672
73	Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala	
74	210 215 220	
75	cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act act	720
76	Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr	
77	225 230 235 240	
78	agt acc ctt cag gaa caa ata gga tgg atg aca cat aat cca cct atc	768
79	Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile	
80	245 250 255	
81	cca gta gga gaa atc tat aaa aga tgg ata atc ctg gga tta aat aaa	816
82	Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys	
83	260 265 270	
84	ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa gga	864
85	Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly	
86	275 280 285	
87	cca aag gaa ccc ttt aga gac tat gta gac cga ttc tat aaa act cta	912
88	Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu	
89	290 295 300	
90	aga gcc gag caa gct tca caa gag gta aaa aat tgg atg aca gaa acc	960
91	Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr	
92	305 310 315 320	
93	ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa gca	1008
94	Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala	

PAGE: 3

RAW SEQUENCE LISTING PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

95		325		330		335		
96	ttg gga cca gga gcg aca cta gaa gaa atg atg aca gca tgt cag gga							1056
97	Leu Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly							
98		340		345		350		
99	gtg ggg gga ccc ggc cat aaa gca aga gtt ttg gct gaa gca atg agc							1104
100	Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser							
101		355		360		365		
102	caa gta aca aat cca gct acc ata atg ata cag aaa ggc aat ttt agg							1152
103	Gln Val Thr Asn Pro Ala Thr Ile Met Ile Gln Lys Gly Asn Phe Arg							
104		370		375		380		
105	aac caa aga aag act gtt aag tgt ttc aat tgt ggc aaa gaa ggg cac							1200
106	Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His							
107		385		390		395		400
108	ata gcc aaa aat tgc agg gcc cct agg aaa aag ggc tgt tgg aaa tgt							1248
109	Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys							
110		405		410		415		
111	gga aag gaa gga cac caa atg aaa gat tgt act gag aga cag gct aat							1296
112	Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn							
113		420		425		430		
114	ttt tta ggg aag atc tgg cct tcc cac aag gga agg cca ggg aat ttt							1344
115	Phe Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe							
116		435		440		445		
117	ctt cag agc aga cca gag cca aca gcc cca cca gaa gag agc ttc agg							1392
118	Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg							
119		450		455		460		
120	ttt ggg gaa gag aca aca act ccc tct cag aag cag gag ccg ata gac							1440
121	Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp							
122		465		470		475		480
123	aag gaa ctg tat cct tta gct tcc ctc aga tca ctc ttt ggc agc gac							1488
124	Lys Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Ser Asp							
125		485		490		495		
126	ccc tcg tca caa taa							1503
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130	<211> LENGTH: 500							
131	<212> TYPE: PRT							
132	<213> ORGANISM: Homo sapien							
133	<400> SEQUENCE: 3							
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136	Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys							
137		20 25 30						
138	His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro							
139		35 40 45						
140	Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu							
141		50 55 60						
142	Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn							
143		65 70 75 80						
144	Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp							

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

145				85				90				95			
146	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys
147				100					105				110		
148	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	Asn	Asn	Ser	Gln
149			115					120					125		
150	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val
151		130						135				140			
152	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val
153	145					150					155				160
154	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu
155				165					170						175
156	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val
157			180						185					190	
158	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu
159			195					200					205		
160	Ala	Ala	Glu	Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile
161		210						215				220			
162	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr
163	225					230					235				240
164	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	His	Asn	Pro	Pro
165				245					250						255
166	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn
167			260						265					270	
168	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln
169			275					280					285		
170	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr
171		290					295					300			
172	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu
173	305					310					315				320
174	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys
175				325						330					335
176	Leu	Gly	Pro	Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln
177			340						345					350	
178	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met
179			355					360					365		
180	Gln	Val	Thr	Asn	Pro	Ala	Thr	Ile	Met	Ile	Gln	Lys	Gly	Asn	Phe
181		370					375					380			
182	Asn	Gln	Arg	Lys	Thr	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly
183	385					390					395				400
184	Ile	Ala	Lys	Asn	Cys	Arg	Ala	Pro	Arg	Lys	Lys	Gly	Cys	Trp	Lys
185				405						410					415
186	Gly	Lys	Glu	Gly	His	Gln	Met	Lys	Asp	Cys	Thr	Glu	Arg	Gln	Ala
187			420						425					430	
188	Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	His	Lys	Gly	Arg	Pro	Gly	Asn
189			435					440					445		
190	Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe
191		450					455					460			
192	Phe	Gly	Glu	Glu	Thr	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile
193	465					470					475				480
194	Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Ser

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999

TIME: 18:41:58

Input Set: I393795.RAW

195		485	490	495	
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198	<210> SEQ ID NO 4				
199	<211> LENGTH: 1503				
200	<212> TYPE: DNA				
201	<213> ORGANISM: Artificial Sequence				
202	<220> FEATURE:				
203	<223> OTHER INFORMATION: Codon optimized form of HIV gag coding region				
204	<220> FEATURE:				
205	<221> NAME/KEY: CDS				
206	<222> LOCATION: (1)...(1503)				
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209	Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp				
210	1 5 10 15				
211	gag aag atc cgc ctg cgc ccc ggc ggc aag aag cag tac aag ctg aag				96
212	Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys				
213	20 25 30				
214	cac atc gtg tgg gcc tcc cgc gag ctg gag cgc ttc gcc gtg aac ccc				144
215	His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro				
216	35 40 45				
217	ggc ctg ctg gag acc tcc gag ggc tgc cgc cag atc ctg ggc cag ctg				192
218	Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu				
219	50 55 60				
220	cag ccc tcc ctg caa acc ggc tcc gag gag ctg cgc tcc ctg tac aac				240
221	Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn				
222	65 70 75 80				
223	acc atc gcc gtg ctg tac tgc gtg cac cag cgc atc gac gtg aag gac				288
224	Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp				
225	85 90 95				
226	acc aag gag gcc ctg gac aag atc gag gag gag cag aac aag tcc aag				336
227	Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys				
228	100 105 110				
229	aag aag gcc cag cag gcc gcc gcc gac acc ggc aac aac tcc cag gtg				384
230	Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val				
231	115 120 125				
232	tcc cag aac tac ccc atc gtg cag aac ctg cag ggc cag atg gtg cac				432
233	Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His				
234	130 135 140				
235	cag gcc atc tcc ccc cgc acc ctg aac gcc tgg gtg aag gtg gtg gag				480
236	Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu				
237	145 150 155 160				
238	gag aag gcc ttc tcc ccc gaa gtc atc ccc atg ttc tcc gcc ctg tcc				528
239	Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser				
240	165 170 175				
241	gag ggc gcc acc ccc cag gac ctg aac acc atg ctg aac acc gtg ggc				576
242	Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly				
243	180 185 190				
244	ggc cac cag gcc gcc atg cag atg ctg aag gag acc atc aac gag gag				624

PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/393,795

DATE: 12/02/1999
TIME: 18:41:58

Input Set: I393795.RAW

Line	? Error/Warning	Original Text
127	W Line data has been corrected	Pro Ser Ser Gln *
302	W Line data has been corrected	Pro Ser Ser Gln *
570	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
898	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
1228	W Line data has been corrected	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A

Input Set: I393795.RAW

Line	Original Text	Corrected Data
127	Pro Ser Ser Gln *	Pro Ser Ser Gln
302	Pro Ser Ser Gln *	Pro Ser Ser Gln
570	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
898	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A
1228	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A	Asp Asp Cys Val Ala Ser Arg Gln Asp Glu A